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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/875,849C

DATE: 10/01/2002

TIME: 15:07:36

Input Set : A:\LKS944A2.txt

Output Set: N:\CRF4\10012002\H875849C.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION.

6 (i) APPLICANT: Briskin, Michael J.
 7 Ringler, Douglas J.
 8 Picarella, Dominic
 9 Newman, Walter

11 (ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
 12 Thereof

14 (iii) NUMBER OF SEQUENCES: 17

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 18 (B) STREET: 530 Virginia Road, PO Box 9133
 19 (C) CITY: Concord
 20 (D) STATE: Massachusetts
 21 (E) COUNTRY: U.S.A.
 22 (F) ZIP: 01742-9133

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
 26 (B) COMPUTER: IBM PC compatible
 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/08/875,849C

C--> 32 (B) FILING DATE: 08-Sep-1997

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: PCT/US96/02153
 37 (B) FILING DATE: 12-FEB-1996
 40 (A) APPLICATION NUMBER: US 08/523,004
 41 (B) FILING DATE: 01-SEP-1995

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Brook, David E.
 45 (B) REGISTRATION NUMBER: 22,592
 46 (C) REFERENCE/DOCKET NUMBER: LKS94-04A2

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: 978-341-0036
 50 (B) TELEFAX: 978-341-0136

60 (2) INFORMATION FOR SEQ ID NO: 1:

62 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 1624 base pairs
 64 (B) TYPE: nucleic acid
 65 (C) STRANDEDNESS: double
 66 (D) TOPOLOGY: linear

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68      (ii) MOLECULE TYPE: cDNA
70      (ix) FEATURE
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 1..1218
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77 ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTI CTG GGG CTC CTC      48
78 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu
79 1 5 10 15
81 CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG      96
82 Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Gln Pro Pro Glu
83 20 25 30
85 CCC GTG GTG GCC GTG GCC TTG GGC GGC TCG CGC CAG CTC ACC TGC CGC      144
86 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
87 35 40 45
89 CTG GCC TGC GCG GAC CGC GGG GGC TCG GTG CAG TGG CGG GGC CTG GAC      192
90 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
91 50 55 60
93 ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC      240
94 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
95 65 70 75 80
97 GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC      288
98 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
99 85 90 95
101 TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CIT GTG TAC      336
102 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
103 100 105 110
105 GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT      384
106 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
107 115 120 125
109 GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC      432
110 Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
111 130 135 140
113 AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG      480
114 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
115 145 150 155 160
119 GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC CAG      528
120 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
121 165 170 175
123 GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CCG CTG CCG      576
124 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
125 180 185 190
127 CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ACC ATG      624
128 Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
129 195 200 205
131 AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC ATC CCC GTC CTG      672
132 Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
133 210 215 220
135 CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT      720
136 His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro

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137 225          230          235          240
139 CCC AAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CCG GAG TCT      768
140 Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
141          245          250          255
143 CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT      816
144 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
145          260          265          270
147 CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT      864
148 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
149          275          280          285
151 CCC GAC AAG ACC TCC CCG GAG CCC GGC CCC CAG CAG GGC TCC ACA CAC      912
152 Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
153          290          295          300
155 ACC CCG AGG AGC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC      960
156 Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser
157 305          310          315          320
159 CAG GCT GGG CCC ACG CAG GGA GAA GIG ATC CCA ACA GGC TCG TCC AAA      1008
160 Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys
161          325          330          335
163 CCI GCG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG      1056
164 Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
165          340          345          350
167 CTG GGA CIG CTG CTC CTG GCC TIG CCC ACG IAT CAC CTC TGG AAA CGC      1104
168 Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
169          355          360          365
171 TGC CGG CAC CTG GCT GAG GAG GAC ACC CAC CCA CCA GCT TCT CTG AGG      1152
172 Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
173          370          375          380
175 CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA AGG GGG ACC GGC CAG      1200
176 Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
177 385          390          395          400
179 GTC GGG ATC AGC CCC TCC TGAGTGGCCA GCCTTTCCCC CTGTGAAAAGC      1248
180 Val Gly Ile Ser Pro Ser
181          405
184 AAAATAGCTT GGACCCCTTC AAGTIGAGAA CTGGTCAGGG CAAACCTGCC TCCCATTCTA      1308
186 CTCAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCCT CTTTGGAGAA      1368
188 GCICATCAGA AACTCAAAAAG AAGGCCACTG TTTGTCTCAC CTACCCATGA CCTGAAGCCC      1428
190 CTCCCTGAGT GGTCCCCACC TTTCIGGACG GAACCACGTA CTTTTTACAT ACATTGATTC      1488
192 ATGTCTCAGC TCTCCCTAAA AATGCGTAAG ACCAAGCTGT GCCCTGACCA CCCTGGGCCC      1548
194 CTGTCTCAGC GACCTCCTGA GGCTTTGGCA AATAAACCTC CTAAAATGAT AAAAAAAAAA      1608
196 AAAAAAAAAA AAAAAA      1624
199 (2) INFORMATION FOR SEQ ID NO: 2:
201 (i) SEQUENCE CHARACTERISTICS:
202 (A) LENGTH: 406 amino acids
203 (B) TYPE: amino acid
204 (D) TOPOLOGY: linear
206 (ii) MOLECULE TYPE: protein
209 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
211 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu

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| | | | | |
|-----|---|-----|-----|-----|
| 212 | 1 | 5 | 10 | 15 |
| 213 | Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu | | | |
| 214 | | 20 | 25 | 30 |
| 217 | Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg | | | |
| 218 | | 35 | 40 | 45 |
| 220 | Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp | | | |
| 221 | | 50 | 55 | 60 |
| 223 | Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr | | | |
| 224 | | 65 | 70 | 75 |
| 226 | Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly | | | |
| 227 | | 85 | 90 | 95 |
| 229 | Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr | | | |
| 230 | | 100 | 105 | 110 |
| 232 | Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly | | | |
| 233 | | 115 | 120 | 125 |
| 235 | Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro | | | |
| 236 | | 130 | 135 | 140 |
| 238 | Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly | | | |
| 239 | | 145 | 150 | 155 |
| 241 | Ala Gln Ala Leu Gly Pro Glu Val Gln Gln Glu Glu Glu Glu Pro Gln | | | |
| 242 | | 165 | 170 | 175 |
| 244 | Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro | | | |
| 245 | | 180 | 185 | 190 |
| 247 | Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met | | | |
| 248 | | 195 | 200 | 205 |
| 250 | Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu | | | |
| 251 | | 210 | 215 | 220 |
| 253 | His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro | | | |
| 254 | | 225 | 230 | 235 |
| 256 | Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser | | | |
| 257 | | 245 | 250 | 255 |
| 259 | Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro | | | |
| 260 | | 260 | 265 | 270 |
| 262 | Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro | | | |
| 263 | | 275 | 280 | 285 |
| 265 | Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His | | | |
| 266 | | 290 | 295 | 300 |
| 268 | Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser | | | |
| 269 | | 305 | 310 | 315 |
| 271 | Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys | | | |
| 272 | | 325 | 330 | 335 |
| 274 | Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val | | | |
| 275 | | 340 | 345 | 350 |
| 277 | Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg | | | |
| 278 | | 355 | 360 | 365 |
| 280 | Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg | | | |
| 281 | | 370 | 375 | 380 |
| 283 | Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln | | | |
| 284 | | 385 | 390 | 395 |
| | | | | 400 |

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286 Val Gly Ile Ser Pro Ser
287          405
290 (2) INFORMATION FOR SEQ ID NO: 3:
292   (i) SEQUENCE CHARACTERISTICS:
293       (A) LENGTH: 1539 base pairs
294       (B) TYPE: nucleic acid
295       (C) STRANDEDNESS: Double
296       (D) TOPOLOGY: linear
298   (ii) MOLECULE TYPE: cDNA
300   (ix) FEATURE:
301       (A) NAME/KEY: CDS
302       (B) LOCATION: 1..1146
306   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
308 ATG GAT TTC GGA CTG GGC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC      48
309 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu
310   1          5          10          15
312 CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG      96
313 Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
314          20          25          30
316 CCG GTG GTG GCG GTG GGC TTG GGC GGC TCG CGC CAG CTC ACC TGC CGC      144
317 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
318          35          40          45
320 CTG GCC TGC GCG GAC CGC GGG GCG TCG GTG CAG TGG CGG GGC CTG GAC      192
321 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
322          50          55          60
324 ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC      240
325 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
326          65          70          75          80
328 GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC      288
329 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
330          85          90          95
332 TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC      336
333 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
334          100          105          110
336 GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT      384
337 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
338          115          120          125
340 GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC      432
341 Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
342          130          135          140
344 AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG      480
345 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
346          145          150          155          160
348 GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG GAG CCC CAG      528
349 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Glu Pro Gln
350          165          170          175
352 GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CCG      576
353 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
354          180          185          190

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